

[First Hit](#) [Fwd Refs](#)[Previous Doc](#)[Next Doc](#)[Go to Doc#](#)

End of Result Set



Generate Collection

Print

L1: Entry 1 of 1

File: USPT

Jul 6, 1999

US-PAT-NO: 5919665

DOCUMENT-IDENTIFIER: US 5919665 A

TITLE: Vaccine for clostridium botulinum neurotoxin

DATE-ISSUED: July 6, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Williams; James A.	Madison	WI		

US-CL-CURRENT: 435/71.1; 435/252.3, 435/320.1, 530/350, 530/825, 536/23.4

CLAIMS:

I claim:

1. A soluble fusion protein comprising a non-toxin protein sequence and a portion of the Clostridium botulinum type A toxin, said portion of the Clostridium botulinum type A toxin comprising a portion of the sequence of SEQ ID NO:28.
2. The fusion protein of claim 1, wherein said portion of the Clostridium botulinum type A toxin sequence comprises SEQ ID NO:23.
3. The fusion protein of claim 1, wherein said non-toxin protein sequence comprises a poly-histidine tract.
4. The fusion protein of claim 3, which comprises SEQ ID NO:26.
5. The fusion protein of claim 1, wherein said fusion protein is substantially endotoxin-free.
6. A host cell containing a recombinant expression vector, said vector encoding a protein comprising at least a portion of a Clostridium botulinum type A toxin protein sequence of SEQ ID NO:28, and wherein said host cell is capable of expressing said protein as a soluble protein in said host cell at a level greater than or equal to 0.75% of the total cellular protein.
7. The host cell of claim 6, wherein said portion of a toxin comprises SEQ ID NO:23.
8. The host cell of claim 6, wherein said fusion protein comprises SEQ ID NO:26.
9. The host cell of claim 6, wherein said host cell is capable of expressing

said protein in said host cell at a level greater than or equal to 20% of the total cellular protein.

10. A soluble fusion protein, comprising at least a portion of Clostridium botulinum C fragment linked to a poly-histidine tag.

[Previous Doc](#)

[Next Doc](#)

[Go to Doc#](#)

 [ExPASy Home page](#)

[Site Map](#)

[Search ExPASy](#)

[Contact us](#)

[Swiss-Prot](#)

Hosted by  [CBR Canada](#) Mirror sites: [Australia](#) [Brazil](#) [Korea](#) [Switzerland](#) [Taiwan](#) [USA](#)

Search  for  

Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: botulinum toxin heavy chain

UniProtKB/Swiss-Prot Release 47.8 of 30-Aug-2005

UniProtKB/TrEMBL Release 30.8 of 30-Aug-2005

updated search 9/05

- Number of sequences found in UniProt Knowledgebase (Swiss-Prot₍₉₎ and TrEMBL₍₁₎): 10
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the [bottom](#) of this page.
- For more directed searches, you can use the Sequence Retrieval System [SRS](#).

Search in UniProtKB/Swiss-Prot: There are matches to 9 out of 192799 entries

BXA1_CLOBO (P10845)

Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain]. {GENE: Name=botA; Synonyms=atx, bna} - Clostridium botulinum

BXA2_CLOBO (Q45894)

Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain]. {GENE: Name=botA; Synonyms=atx, bna} - Clostridium botulinum

BXB_CLOBO (P10844)

Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BoNT/B) (Bontoxilysin B) [Contains: Botulinum neurotoxin B light chain; Botulinum neurotoxin B heavy chain]. {GENE: Name=botB} - Clostridium botulinum

BXC1_CLOBO (P18640)

Botulinum neurotoxin type C1 precursor (EC 3.4.24.69) (BoNT/C1) (Bontoxilysin C1) [Contains: Botulinum neurotoxin C1 light chain; Botulinum neurotoxin C1 heavy chain]. - Clostridium botulinum

BXD_CLOBO (P19321)

Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BoNT/D) (Bontoxilysin D) [Contains: Botulinum neurotoxin D light chain; Botulinum neurotoxin D heavy chain]. {GENE: Name=botD} - Clostridium botulinum

BXE_CLOBO (Q00496)

Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E) (Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain; Botulinum neurotoxin E heavy chain]. - Clostridium botulinum

BXE_CLOBU (P30995)

Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E) (Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain; Botulinum neurotoxin E heavy chain]. - Clostridium butyricum

BXF CLOBO (P30996)

Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BoNT/F) (Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain; Botulinum neurotoxin F heavy chain]. {GENE: Name=botF} - Clostridium botulinum

BXG CLOBO (Q60393)

Botulinum neurotoxin type G precursor (EC 3.4.24.69) (BoNT/G) (Bontoxilysin G) [Contains: Botulinum neurotoxin G light chain; Botulinum neurotoxin G heavy chain]. {GENE: Name=botG} - Clostridium botulinum

Search in UniProtKB/TrEMBL: There are matches to 1 out of 1973644 entries

Q9R540 CLOBO

Neurotoxin heavy chain 18 kDa fragment (Fragment) - Clostridium botulinum

New Search

in Swiss-Prot/TrEMBL by AC, ID, description,
gene name, organism

**Please do NOT use any boolean operators (and,
or, etc.)**

If you would like to retrieve all the Swiss-Prot/TrEMBL entries contained in this list, you can enter a file name. These entries will then be saved to a file under this name in the directory outgoing of the ExPASy anonymous ftp server, from where you can download it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: ☒ Swiss-Prot ☐ Fasta

Reset

or

Create file

 [ExPASy Home page](#)

[Site Map](#)

[Search ExPASy](#)

[Contact us](#)

[Swiss-Prot](#)

Hosted by  [CBR Canada](#) Mirror sites: [Australia](#) [Brazil](#) [Korea](#) [Switzerland](#) [Taiwan](#) [USA](#)

sp P10845 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA1_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 862 bits (2227), Expect = 0.0

Identities = 422/423 (99%), Positives = 422/423 (99%), Gaps = 1/423 (0%)

Query: 1 INTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 INTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
 Sbjct: 873 INTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 932

Query: 61 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI
 Sbjct: 933 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 992

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 KQRVVFYKYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
 Sbjct: 993 KQRVVFYKYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 1052

Query: 181 MFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM 240
 MFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM
 Sbjct: 1053 MFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM 1112

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI
 Sbjct: 1113 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 1172

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ-VVMKSKNDQGITN 359
 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ VVMKSKNDQGITN
 Sbjct: 1173 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 1232

Query: 360 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGC SWEFIPVDDGWGE 419
 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGC SWEFIPVDDGWGE
 Sbjct: 1233 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGC SWEFIPVDDGWGE 1292

Query: 420 RPL 422
 RPL
 Sbjct: 1293 RPL 1295

tr Q7B8V4 BoNT/A (Neurotoxin BoNT) [bont/a] [Clostridium 1296
 Q7B8V4_CLOBO botulinum] AA
 align

Score = 862 bits (2227), Expect = 0.0

Identities = 422/423 (99%), Positives = 422/423 (99%), Gaps = 1/423 (0%)

Query: 1 INTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 INTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
 Sbjct: 874 INTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 933

Query: 61 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI
 Sbjct: 934 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 993

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
 Sbjct: 994 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 1053

Query: 181 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYM 240
 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYM
 Sbjct: 1054 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYM 1113

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI 300
 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI
 Sbjct: 1114 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI 1173

Query: 301 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQ-VVMKSKNDQGITN 359
 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQ VVMKSKNDQGITN
 Sbjct: 1174 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 1233

Query: 360 KCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGCSEWEIFVDDGWGE 419
 KCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGCSEWEIFVDDGWGE
 Sbjct: 1234 KCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGCSEWEIFVDDGWGE 1293

Query: 420 RPL 422
 RPL
 Sbjct: 1294 RPL 1296

sp Q45894 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA2_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 759 bits (1960), Expect = 0.0
 Identities = 367/423 (86%), Positives = 396/423 (92%), Gaps = 1/423 (0%)

Query: 1 INTSILNLRYESNHLIDL SRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 +NTSIL++ Y+ + LIDLSRY +KINIG +V +D IDKNQI+L NLESS IEVILKNAIV
 Sbjct: 873 VNTSILSIVYKKDDLIDL SRYGAKINIGDRVYYSIDKNQIKLINLESSTIEVILKNAIV 932

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWI+IPKYF+ I+LNNEYTIINC+ENNSGWKVSLNYGEIIWTLQD ++
 Sbjct: 933 YNSMYENFSTSFWIKIPKYFSKINLNNEYTIINCIENNSGWKVSLNYGEIIWTLQDNKQN 992

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 QRVVFYKYSQM+NISDYINRWIFVTITNNRL SKIYINGRLIDQKPISNLGNIHASN I
 Sbjct: 993 IQRVVFYKYSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKI 1052

Query: 181 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYM 240
 MFKLDGCRD RYI IKYFNLFDKELNEKEIKDLYD+QSN SGILKDFWG+YLQYDKPYM
 Sbjct: 1053 MFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSN SGILKDFWGNLYLYQYDKPYM 1112

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI 300
 LNL+DPNKYVDVNN+GIRGYMYLKGPRGSV+TTNIYLN+LY GTKFIKKYASGN+DNI
 Sbjct: 1113 LNLFDPNKYVDVNNIGIRGYMYLKGPRGSVVTTNIYLNSTLYEGTKFIKKYASGNEDNI 1172

Query: 301 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQ-VVMKSKNDQGITN 359
 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQ VVMKSK+DQGI N

Sbjct: 1173 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRN 1232

Query: 360 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYNQIERSSRTLGCSEFIPVDDGWGE 419
KCKMNLQDNNNGNDIGFIGFH ++NIAKLVASNWNRYNQ+ ++SRT GCSWEFIPVDDGWGE

Sbjct: 1233 KCKMNLQDNNNGNDIGFIGFHLVDNIAKLVASNWNRYNQVGKASRTFGCSWEFIPVDDGWGE 1292

Query: 420 RPL 422
L

Sbjct: 1293 SSL 1295

tr Q58GH1 Type A2 botulinum neurotoxin [Clostridium botulinum] 1296 AA
Q58GH1_CLOBO

align

Score = 759 bits (1960), Expect = 0.0

Identities = 367/423 (86%), Positives = 396/423 (92%), Gaps = 1/423 (0%)

Query: 1 INTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
+NTSIL++ Y+ + LIDLRY +KINIG +V +D IDKNQI+L NLESS IEVILKNAIV

Sbjct: 874 VNTSILSIVYKKDDLIDLRYGAKINIGDRVYYSIDKNQIKLINLESSTIEVILKNAIV 933

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINC MENNSGWKVS LNYGEIIWTLQDTQEI 120
YNSMYENFSTSFWI+IPKYF+ I+LNNEYTIINC+ENNSGWKVS LNYGEIIWTLQD ++

Sbjct: 934 YNSMYENFSTSFWIKIPKYFSKINLNNEYTIINCIENNSGWKVS LNYGEIIWTLQDNKQN 993

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
QRVVFYKYSQM+NISDYINRWIFVTITNNRL SKIYINGRLIDQKPISNLGNIHASN I

Sbjct: 994 IQRVVFYKYSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKI 1053

Query: 181 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYYM 240
MFKLDGCRD RYI IKYFNLFDKELNEKEIKDLYD+QSN SGILKDFWG+YLQYDKPYYM

Sbjct: 1054 MFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSN SGILKDFWGNLYQYDKPYYM 1113

Query: 241 LNLDPN KYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI 300
LNL+DPN KYVDVNN+GIRGYMYLKGPRGSV+TTNIYLN S+LY GTKFIKKYASGN+DNI

Sbjct: 1114 LNLDPN KYVDVNNIGIRGYMYLKGPRGSVTTNIYLNSTLYEGTKFIKKYASGNEDNI 1173

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ-VVMKSKNDQGITN 359
VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ VVMKSK+DQGI N

Sbjct: 1174 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRN 1233

Query: 360 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYNQIERSSRTLGCSEFIPVDDGWGE 419
KCKMNLQDNNNGNDIGFIGFH ++NIAKLVASNWNRYNQ+ ++SRT GCSWEFIPVDDGWGE

Sbjct: 1234 KCKMNLQDNNNGNDIGFIGFHLVDNIAKLVASNWNRYNQVGKASRTFGCSWEFIPVDDGWGE 1293

Query: 420 RPL 422
L

Sbjct: 1294 SSL 1296

tr Q57236 BoNT/F (Neurotoxin type F) [bont/f] [Clostridium 1278
Q57236_CLOBO botulinum] AA
align

Score = 417 bits (1073), Expect = e-115

Identities = 211/423 (49%), Positives = 285/423 (66%), Gaps = 18/423 (4%)

```

Query: 2      NTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY 61
              + SIL++RYE+N ID+S Y S I+I V ++NQ +++ + S++ + N I+Y
Sbjct: 868    DNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVNIAQNNDIY 927

Query: 62     NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENN-SGWKVSLNYGEIIWTLQDTQEI 120
              N Y+NFS SFW+RIPKYFN ++LNNEYTII+C+ NN SGWK+SLNY +IIWTLQDT
Sbjct: 928    NGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGN 987

Query: 121    KQRVVFYKYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
              Q++VF Y+QMI+ISDYIN+WIFVTITNRL NS+IYING LID+K ISNLG+IH S+NI
Sbjct: 988    NQKLVFNYSQMINISDYINKWIFVTITNRLGNSRIYINGNLIDEKSSISNLGDIHVSDNI 1047

Query: 181    MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNISGILKDFWGDYLYQDKPYM 240
              +FK+ GC DT RY+ I+YF +FD EL + EI+ LY ++ + ILKDFWG+YL Y+K YY+
Sbjct: 1048    LFKIVGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNLYLLYNKRYYL 1106

Query: 241    LNLDPNPKYVDVNNVVGIRGYMYLKGPRGSMVTNIYLNSSLYRGTKFIIKKYAS---GNK 297
              LNL +K + N+ ++ + RG NI+ N+ LY G + II+K S N
Sbjct: 1107    LNLRLTDKSTQNS----NFLNINQQRGVYQKPNIFSNTRLTYTGVEVIIRKNGSTDISNT 1162

Query: 298    DNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGN-LSQVVMKSKNDQG 356
              DN VR ND YINVV ++ EYRL + S A EKI+ + + N L Q+++
Sbjct: 1163    DNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNNSNLSLQGIIVM----DS 1218

Query: 357    ITNKCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWYNRQIERSSRTLGCSEFIPVDDG 416
              I N C MN Q+NNG +IG +GFH N LVAS+WY I +++ + GC W FI + G
Sbjct: 1219    IGNNCTMNFQNNNGGNIGLLGFHSNN---LVASSWYNNIRKNTSSNGCFWSFISKEHG 1274

Query: 417    WGE 419
              W E
Sbjct: 1275    WQE 1277

```

```

tr   Q45851      Neurotoxin type F [bont /f] [Clostridium      1268 AA
      Q45851_9CLOT baratii]                                align

```

Score = 416 bits (1070), Expect = e-115

Identities = 214/424 (50%), Positives = 281/424 (65%), Gaps = 18/424 (4%)

```

Query: 1      INTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
              I++SILN++YE+N ID S Y S I+I + ++NQ +++ S++ + N I+
Sbjct: 858    IDSSILNMKYENNRFDSSGYGSNISINGDIYIYSTNRNQFGIYSSRLSEVNITQNNTII 917

Query: 61     YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENN-SGWKVSLNYGEIIWTLQDTQE 119
              YNS Y+NFS SFW+RIPKY N +LNNEYTIINCM NN SGWK+SLNY IIWTLQDT
Sbjct: 918    YNSRYQNFSVSFWVRIPKYNNLKNLNNEYTIINCMRNNNSGWKISLNYNNIIWTLQDTTG 977

Query: 120    IKQRVVFYKYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNN 179
              Q++VF Y+QMI+ISDYIN+W FVTITNRL +SK+YING L DQK I NLGNIH +N
Sbjct: 978    NNQKLVFNYSQMINISDYINKWTFVTITNRLGHSKLYINGNLTDQKSILNLGNIHVDDN 1037

Query: 180    IMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNISGILKDFWGDYLYQDKPYY 239
              I+FK+ GC DT RY+ I+YF +F+ EL++ EI+ LY ++ +S ILKDFWG+YL Y+K YY

```

Sbjct: 1038 ILFKIVGCNDT-RYVGIRYFKIFNMELDKTEIETLYHSEPDSTILKDFWGNLYLLYNKKYY 1096

Query: 240 MLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYAS---GN 296
+LNL PN V N+ + + RG TNI+ N+ LY G + II+K S N

Sbjct: 1097 LLNLLKPNMSVTKNS---DILNINRQIRGIYSKTNIFSNARLYTGVEVIIRKVGSTDTSN 1152

Query: 297 KDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVG-NLSQVVMKSKNDQ 355
DN VR ND VYINVV N EY+L + S + VEK + I + N +Q+++

Sbjct: 1153 TDNFVRKNDTVYINVVDGNSEYQLYADVSTSAVEKTIKLRRISNSNYNSNQMIIM---D 1208

Query: 356 GITNKCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEFIPVDD 415
I + C MN + NNGNDIG +GFH N LVAS+WY + I ++R GC W FI +

Sbjct: 1209 SIGDNCTMNFKTNNNGNDIGLLGFHLNN---LVASSWYKNIIRNNTNRNGCFWSFISKEH 1264

Query: 416 GWGE 419
GW E

Sbjct: 1265 GWQE 1268

tr Q9K395 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1251 AA
Q9K395_CLOBU align

Score = 379 bits (974), Expect = e-104
Identities = 200/431 (46%), Positives = 273/431 (62%), Gaps = 40/431 (9%)

Query: 2 NTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY 61
++S+LN+RY+++ +D S Y S INI ++ P +KNQ +FN + S++ + + I+Y

Sbjct: 849 SSSVLNMRKYKNDKYVDTSGYDSNININGEIFIYPTNKNQFTIFNSKPSEVNISQNDYIIY 908

Query: 62 NSMYENFSTSFWIRIPKYFNSI-SLNNEYTIINC-M-ENNSGWKVSLNYGEIIWTLQDTQE 119
++ Y+NFS SEW+RIP Y N I ++NNEYTIINC-M-ENNSGWKVSLN+ EIIWTLQD

Sbjct: 909 DNKYKNFSISFWVRIPNYDNKIVNINNEYTIINC-MRDNNSGWKVSLNHNEIIWTLQDNAR 968

Query: 120 IKQRVVFKYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNN 179
I Q++VFKY ISDYIN+WIFVTITN+RL +SK+YING LIDQK I NLGNIH S+N

Sbjct: 969 INQKLVFKYGNANGISDYINKWIFVTITNDRLGDSKLYINGHLIDQKSILNLGNIHVSDN 1028

Query: 180 IMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNKGILKDFWGDYLYDKPYY 239
I+FK+ C T RYI I+YFN+FDKEL+E EI+ LY N+ N+ ILKDFWG+YL YDK YY

Sbjct: 1029 ILFKIVNCSYT-RYIGIRYFNIFDKELDETEIQTLYSNEPNTNILKDFWGNLYLLYDKGY 1087

Query: 240 MLNLYDPNKYVD-----VNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKK 291
+LN+ PN ++D +NN+ + I L + LY G K I++

Sbjct: 1088 LLNVLPNNFIDRRKDSTLSINNI-----RSTILLANRLYSGIKVKIQR 1131

Query: 292 Y-ASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVG-NLSQVVM 349
S D VR ND+VYIN + Y L + + EK + + GN +QVV+

Sbjct: 1132 VNDSSSTNDRFVRKNDQVYINYISNSSSYSLYADTNTTDEKTIKS---SSSGNRNFNQVVV 1188

Query: 350 KSKNDQGKITNKCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSE 409
+ + N C MN ++NNGN+IG +GF +VAS WY + + + GC W

Sbjct: 1189 MN----SVGNCTMNFKNNGNNGNIGLLGF----KADTVVASTWYYTHMRDHTNSNGCFWN 1240

Query: 410 FIPVDDGWGER 420
FI + GW E+

Sbjct: 1241 FISEEHGWQEK 1251

tr Q9ZAJ5 BonT protein [bonT] [Clostridium 1280 AA
Q9ZAJ5_CLOBO botulinum] align

Score = 379 bits (973), Expect = e-104

Identities = 196/426 (46%), Positives = 276/426 (64%), Gaps = 21/426 (4%)

Query: 2 NTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY 61
++SIL++RYE+N ID+S Y S I+I V ++NQ +++ S++ + N I+Y
Sbjct: 868 DSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQFGIYSGRLSEVNIAQNNDIIY 927

Query: 62 NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVS LNY---GEIIWTLQDT 117
NS Y+NFS SFW+ IPK++ ++ N EYTIINCM NNSGWK+SL EIIWTLQDT
Sbjct: 928 NSRYQNFSISFWVTIPKHYRPMNRNREYTIINCMGNNSGWKISLRTIRDCEIIWTLQDT 987

Query: 118 QEIKQRVVFVKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHAS 177
K++++F+Y ++ +ISDYIN+WIFVTITNNRL NS+IYING LI +K ISNLG+IH S
Sbjct: 988 SGNKEKLIFRYEELASISDYINKWIFVTITNNRLGNSRIYINGNLIVEKSISNLGDIHVS 1047

Query: 178 NNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKP 237
+NI+FK+ GC D Y+ I+YF +F+ EL++ EI+ LY N+ + ILKD+WG+YL Y+K
Sbjct: 1048 DNILFKIVGC-DDETYVGIRYFKVFNTELDKEIETLYSNEPDPSILKDYWGNYLLYNKK 1106

Query: 238 YYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYAS--- 294
YY+ NL +KY+ N+ G + + RG +++LN LY G + II+K A
Sbjct: 1107 YYLFNLLRKDKYITRNS----GILNINQQRGVTGGISVFLNYKLYEGVEVIIRKNAPIDI 1162

Query: 295 GNKDNIVRNNDRVYINVVVNKEYRLATNASQAGVEKILSALEIPDVG-NLSQVVMKSKN 353
N DN VR ND YINVV EYRL + S EKI+ + + +L Q+++
Sbjct: 1163 SNTDNFVRKNLDLAYINVVDHGVEYRLYADISITKSEKIIKLIRTSNPNDSLGQIIIVM--- 1219

Query: 354 DQGITNKCKMNLQDNNNGNDIGFIGFHQFNNAIKLVASNWNRYQIERSSRTLGCSEWFIPV 413
I N C MN Q+N+G++IG +GFH + LVAS+WY I R++ + GC W FI
Sbjct: 1220 -DSIGNNCTMNFQNNDGSGNIGLLGFHSDD----LVASSWYNNHIRRNTSSNGCFWSFISK 1274

Query: 414 DDGWGE 419
+ GW E
Sbjct: 1275 EHWKE 1280

sp P30996 Botulinum neurotoxin type F precursor (EC 3.4.24.69) 1274
BXF_CLOBO (BoNT/F) AA
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light align
chain; Botulinum neurotoxin F heavy chain] [botF]
[Clostridium botulinum]

Score = 377 bits (968), Expect = e-103

Identities = 197/425 (46%), Positives = 279/425 (65%), Gaps = 24/425 (5%)

Query: 2 NTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY 61
++SIL++RYE+N ID+S Y S I+I V ++NQ ++N S++ + N I+Y
Sbjct: 867 DSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQFGIYNSRLSEVNIAQNNDIIY 926

Query: 62 NSMYENFSTSFWIRIPKYFNSISLNN EYTIINCM-ENNSGWKVSLNYG---EIIWTLQDT 117
NS Y+NFS SFW+RIPK++ ++ N EYTIINCM NNSGWK+SL EIIWTLQDT
Sbjct: 927 NSRYQNFSISFWVRIPKHYKPMNHNREYTIINCMGNNNSGWKISLRTVRDCEIIWTLQDT 986

Query: 118 QEIKQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHAS 177
K+ ++F+Y ++ IS+YIN+WIFVTITNNRL NS+IYING LI +K ISNLG+IH S
Sbjct: 987 SGNKENLIFRYEELNRISNYINKWIFVTITNNRLGNSRIYINGNLIVEKSISNLGDIHVS 1046

Query: 178 NNIMFKLDGCRDTHRYIWIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKP 237
+NI+FK+ GC D Y+ I+YF +F+ EL++ EI+ LY N+ + ILK++WG+YL Y+K
Sbjct: 1047 DNILFKIVGC-DEETYVGIRYFKVFNTLDTKEIETLYSNEPDPSILKNYWGNYLLYNKK 1105

Query: 238 YYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYAS--- 294
YY+ NL +KY+ +N+ G + + RG V +++LN LY G + II+K
Sbjct: 1106 YYLFNLLRKDKYITLNS---GILNINQQRG-VTEGSVFLNYKLYEGVEVIIRKNGPIDI 1160

Query: 295 GNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKND 354
N DN VR ND YINVV + EYRL + +++ EKI+ + D +L Q+++
Sbjct: 1161 SNTDNFVRKNDLAYINVVDRGVEYRLYAD-TKSEKEKIIRTSNLND--SLGQIIVM---- 1213

Query: 355 QGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSEWIFIPVD 414
I N C MN Q+NNG++IG +GFH N LVAS+WY I R++ + GC W I +
Sbjct: 1214 DSI GNNCTMNFQNNNGSNIGLLGFHSNN---LVASSWYNNIRNTSSNGCFWSSISKE 1269

Query: 415 DGWGE 419
+GW E
Sbjct: 1270 NGWKE 1274

Db AC	Description	Score	E-value
<input checked="" type="checkbox"/> sp P10845	BXA1_CLOBO Botulinum neurotoxin type A precursor (EC 3...	862	0.0
<input checked="" type="checkbox"/> tr Q7B8V4	_CLOBO BoNT/A (Neurotoxin BoNT) [bont/a] [Clostridium b...	862	0.0
<input checked="" type="checkbox"/> sp Q45894	BXA2_CLOBO Botulinum neurotoxin type A precursor (EC 3...	759	0.0
<input checked="" type="checkbox"/> tr Q58GH1	_CLOBO Type A2 botulinum neurotoxin [Clostridium botuli...	759	0.0

CLUSTAL W (1.82) multiple sequence alignment

```

sp|P10845|BXA1_CLOBO      -PFVNKQFNYPKDPVNGVDIAYIKIPNVGQMQPVKAFKIHNKIWWIPERDT
tr|Q7B8V4|Q7B8V4_CLOBO  MPFVNKQFNYPKDPVNGVDIAYIKIPNAGQMQPVKAFKIHNKIWWIPERDT
sp|Q45894|BXA2_CLOBO      -PFVNKQFNYPKDPVNGVDIAYIKIPNAGQMQPVKAFKIHNKIWWIPERDT
tr|Q58GH1|Q58GH1_CLOBO  MPFVNKQFNYPKDPVNGVDIAYIKIPNAGQMQPVKAFKIHNKIWWIPERDT
                          *****

sp|P10845|BXA1_CLOBO      FTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYKGVTKLFERIYS
tr|Q7B8V4|Q7B8V4_CLOBO  FTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYKGVTKLFERIYS
sp|Q45894|BXA2_CLOBO      FTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYKGVTKLFERIYS
tr|Q58GH1|Q58GH1_CLOBO  FTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYKGVTKLFERIYS
                          *****

sp|P10845|BXA1_CLOBO      TDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELN
tr|Q7B8V4|Q7B8V4_CLOBO  TDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELN
sp|Q45894|BXA2_CLOBO      TDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELN
tr|Q58GH1|Q58GH1_CLOBO  TDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELN
                          *****

sp|P10845|BXA1_CLOBO      LVIIGPSADIIQFECKSFGHEVLNLTNRNGYGSTQYIRFSPDFTFGFEESL
tr|Q7B8V4|Q7B8V4_CLOBO  LVIIGPSADIIQFECKSFGHEVLNLTNRNGYGSTQYIRFSPDFTFGFEESL
sp|Q45894|BXA2_CLOBO      LVIIGPSADIIQFECKSFGHVDLNLTRNGYGSTQYIRFSPDFTFGFEESL
tr|Q58GH1|Q58GH1_CLOBO  LVIIGPSADIIQFECKSFGHVDLNLTRNGYGSTQYIRFSPDFTFGFEESL
                          *****

sp|P10845|BXA1_CLOBO      EVDTNPLLGAAGKATDPAVTLAHELIHAGHRLYGIAINPNRVFKVNTNAY
tr|Q7B8V4|Q7B8V4_CLOBO  EVDTNPLLGAAGKATDPAVTLAHELIHAGHRLYGIAINPNRVFKVNTNAY
sp|Q45894|BXA2_CLOBO      EVDTNPLLGAAGKATDPAVTLAHELIHAEHRLYGIAINPNRVFKVNTNAY
tr|Q58GH1|Q58GH1_CLOBO  EVDTNPLLGAAGKATDPAVTLAHELIHAEHRLYGIAINPNRVFKVNTNAY
                          *****

sp|P10845|BXA1_CLOBO      YEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKA
tr|Q7B8V4|Q7B8V4_CLOBO  YEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKA
sp|Q45894|BXA2_CLOBO      YEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKA
tr|Q58GH1|Q58GH1_CLOBO  YEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKA
                          *****

sp|P10845|BXA1_CLOBO      KSIIGTTASLQYMKNVFKKYLLEDTSKGFSVDKLFKDKLYKMLTEIYT
tr|Q7B8V4|Q7B8V4_CLOBO  KSIIGTTASLQYMKNVFKKYLLEDTSKGFSVDKLFKDKLYKMLTEIYT
sp|Q45894|BXA2_CLOBO      KSIIGTTASLQYMKNVFKKYLLEDTSKGFSVDKLFKDKLYKMLTEIYT
tr|Q58GH1|Q58GH1_CLOBO  KSIIGTTASLQYMKNVFKKYLLEDTSKGFSVDKLFKDKLYKMLTEIYT
                          ***

sp|P10845|BXA1_CLOBO      EDNFVKFFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLNNTNLAAN
tr|Q7B8V4|Q7B8V4_CLOBO  EDNFVKFFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLNNTNLAAN
sp|Q45894|BXA2_CLOBO      EDNFVNFFKVINRKYTLNFDKAVFRINIVPDENYTIKDGFNKLGANLSTN
tr|Q58GH1|Q58GH1_CLOBO  EDNFVNFFKVINRKYTLNFDKAVFRINIVPDENYTIKDGFNKLGANLSTN
                          *****

sp|P10845|BXA1_CLOBO      FNGQNTTEINNMNFTKLKNFTGLFEFYKLLCVRGIIITSKTKSLDKGYNKAL
tr|Q7B8V4|Q7B8V4_CLOBO  FNGQNTTEINNMNFTKLKNFTGLFEFYKLLCVRGIIITSKTKSLDKGYNKAL
sp|Q45894|BXA2_CLOBO      FNGQNTTEINSRNFTRLKNFTGLFEFYKLLCVRGIIIPFKTKSLDEGYNKAL
tr|Q58GH1|Q58GH1_CLOBO  FNGQNTTEINSRNFTRLKNFTGLFEFYKLLCVRGIIIPFKTKSLDEGYNKAL
                          *****

sp|P10845|BXA1_CLOBO      NDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSNTNIEAAEENISLDLIQ
tr|Q7B8V4|Q7B8V4_CLOBO  NDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSNTNIEAAEENISLDLIQ
sp|Q45894|BXA2_CLOBO      NDLCIKVNNWDLFFSPSEDNFTNDLDKVEEITADTNIEAAEENISLDLIQ

```

tr Q58GH1 Q58GH1_CLOBO	NDLCIKVNNDLFFSPSEDNFTNDLDKVEEITADTNIEAAEENISLDLIQ *****.* ****.******
sp P10845 BXA1_CLOBO	QYYLTFNFDNEPENISIE NLSSDIIGQLELMPNIERFPNGKKYELDKYTM
tr Q7B8V4 Q7B8V4_CLOBO	QYYLTFNFDNEPENISIE NLSSDIIGQLELMPNIERFPNGKKYELDKYTM
sp Q45894 BXA2_CLOBO	QYYLTFDFDNEPENISIE NLSSDIIGQLEPMPNIERFPNGKKYELDKYTM
tr Q58GH1 Q58GH1_CLOBO	QYYLTFDFDNEPENISIE NLSSDIIGQLEPMPNIERFPNGKKYELDKYTM *****.******
sp P10845 BXA1_CLOBO	FHYLRAQEFEGHKSRIALTNSVNEALLNPSRVYTFSSDYVKKVKNKATEA
tr Q7B8V4 Q7B8V4_CLOBO	FHYLRAQEFEGHKSRIALTNSVNEALLNPSRVYTFSSDYVKKVKNKATEA
sp Q45894 BXA2_CLOBO	FHYLRAQEFEGHDSRIILTNSAEEALLKPNVAYTFSSKYVKKINKAVEA
tr Q58GH1 Q58GH1_CLOBO	FHYLRAQEFEGHDSRIILTNSAEEALLKPNVAYTFSSKYVKKINKAVEA *****.* ****.*:****.*.*****.****.*:***.*
sp P10845 BXA1_CLOBO	AMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKD
tr Q7B8V4 Q7B8V4_CLOBO	AMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKD
sp Q45894 BXA2_CLOBO	FMFLNWAEELVYDFTDETNEVTTMDKIADITIIIPYIGPALNIGNMLSKG
tr Q58GH1 Q58GH1_CLOBO	FMFLNWAEELVYDFTDETNEVTTMDKIADITIIIPYIGPALNIGNMLSKG ***.*.*:*****.*:* *****.******.*
sp P10845 BXA1_CLOBO	DFVGALIFSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTQVOTIDNALS
tr Q7B8V4 Q7B8V4_CLOBO	DFVGALIFSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTQVOTIDNALS
sp Q45894 BXA2_CLOBO	EFVEAIIFTGVVAMLEFIPEYALPVFGTFAIVSYIANKVLTQVOTINNALS
tr Q58GH1 Q58GH1_CLOBO	EFVEAIIFTGVVAMLEFIPEYALPVFGTFAIVSYIANKVLTQVOTINNALS :* *:*:*.*.* :***** *:*:*:*:*:*:*:*:*:*:*:*:*:*:*
sp P10845 BXA1_CLOBO	KRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEALENQAEATKAIINYQ
tr Q7B8V4 Q7B8V4_CLOBO	KRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEALENQAEATKAIINYQ
sp Q45894 BXA2_CLOBO	KRNEKWDEVYKYIVTNWLAKVNTQIDLIREKMKKALENQAEATKAIINYQ
tr Q58GH1 Q58GH1_CLOBO	KRNEKWDEVYKYIVTNWLAKVNTQIDLIREKMKKALENQAEATKAIINYQ *****.* *****.*:***.******
sp P10845 BXA1_CLOBO	YNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSM
tr Q7B8V4 Q7B8V4_CLOBO	YNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSM
sp Q45894 BXA2_CLOBO	YNQYTEEEKNNINFNIDDLSSKLNESINSAMININKFLDQCSVSYLMNSM
tr Q58GH1 Q58GH1_CLOBO	YNQYTEEEKNNINFNIDDLSSKLNESINSAMININKFLDQCSVSYLMNSM *****.******.******.******
sp P10845 BXA1_CLOBO	IPYGVKRLDFDASLKDALLKYIYDNRGTLIGQVDRLKDKVNNTLSTDIP
tr Q7B8V4 Q7B8V4_CLOBO	IPYGVKRLDFDASLKDALLKYIYDNRGTLIGQVDRLKDKVNNTLSTDIP
sp Q45894 BXA2_CLOBO	IPYAVKRLKDFDASVRDVLLKYIYDNRGTLVLQVDRLKDEVNNTLSADIP
tr Q58GH1 Q58GH1_CLOBO	IPYAVKRLKDFDASVRDVLLKYIYDNRGTLVLQVDRLKDEVNNTLSADIP ***.******.*:*****.*:*****.*:*****.*:***
sp P10845 BXA1_CLOBO	FQLSKYVDNQRLLSFTFEYIKNIINTSILNLRYESNHLIDL SRYASKINI
tr Q7B8V4 Q7B8V4_CLOBO	FQLSKYVDNQRLLSFTFEYIKNIINTSILNLRYESNHLIDL SRYASKINI
sp Q45894 BXA2_CLOBO	FQLSKYVDNKKLLSFTFEYIKNIVNTSILSIVYKKDDLIDL SRYGAKINI
tr Q58GH1 Q58GH1_CLOBO	FQLSKYVDNKKLLSFTFEYIKNIVNTSILSIVYKKDDLIDL SRYGAKINI *****.*:*****.*:*****.*: *::.******.*:****
sp P10845 BXA1_CLOBO	GSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVNSMYENFSTSFWIRIP
tr Q7B8V4 Q7B8V4_CLOBO	GSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVNSMYENFSTSFWIRIP
sp Q45894 BXA2_CLOBO	GDRVYYSIDKNQIKLINLESSTIEVILKNAIVNSMYENFSTSFWIKIP
tr Q58GH1 Q58GH1_CLOBO	GDRVYYSIDKNQIKLINLESSTIEVILKNAIVNSMYENFSTSFWIKIP *.:* *:*.******.*:*****.******.******.*:***
sp P10845 BXA1_CLOBO	KYFNSISLNNEYTIINC MENSGWKVSLNYGEIIWTLQDTQEIKQRVVFK
tr Q7B8V4 Q7B8V4_CLOBO	KYFNSISLNNEYTIINC MENSGWKVSLNYGEIIWTLQDTQEIKQRVVFK
sp Q45894 BXA2_CLOBO	KYFSKINLNNEYTIINCIENSGWKVSLNYGEIIWTLQDNKQNIQRVVFK

tr Q58GH1 Q58GH1_CLOBO	KYFSKINLNNYEYTIINCIENN SGWKVSLNYGEIIWTLQDNKQNIQRVVF ***. *.*****:*****.***
sp P10845 BXA1_CLOBO	YSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHAS
tr Q7B8V4 Q7B8V4_CLOBO	YSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHAS
sp Q45894 BXA2_CLOBO	YSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHAS
tr Q58GH1 Q58GH1_CLOBO	YSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHAS ****:*****.***:*****
sp P10845 BXA1_CLOBO	NNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDF
tr Q7B8V4 Q7B8V4_CLOBO	NNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDF
sp Q45894 BXA2_CLOBO	NKIMFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSN SGILKDF
tr Q58GH1 Q58GH1_CLOBO	NKIMFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSN SGILKDF *:*****.*** *****
sp P10845 BXA1_CLOBO	WGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGRGSMVTNNIYL
tr Q7B8V4 Q7B8V4_CLOBO	WGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGRGSMVTNNIYL
sp Q45894 BXA2_CLOBO	WGNYLQYDKPYYMLNLYDPNKYVDVNNIGIRGYMYLKGRGSMVTNNIYL
tr Q58GH1 Q58GH1_CLOBO	WGNYLQYDKPYYMLNLYDPNKYVDVNNIGIRGYMYLKGRGSMVTNNIYL **.:*****:*****:*****
sp P10845 BXA1_CLOBO	NSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQA
tr Q7B8V4 Q7B8V4_CLOBO	NSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQA
sp Q45894 BXA2_CLOBO	NSTLYEGTKFIIKKYASGNEDNIVRNNDRVYINVVVKNKEYRLATNASQA
tr Q58GH1 Q58GH1_CLOBO	NSTLYEGTKFIIKKYASGNEDNIVRNNDRVYINVVVKNKEYRLATNASQA **.:**.:*****:*****
sp P10845 BXA1_CLOBO	GVEKILSALEIPDVGNLSQVVMKSKNDQGITNKCKMNLQDNNGNDIGFI
tr Q7B8V4 Q7B8V4_CLOBO	GVEKILSALEIPDVGNLSQVVMKSKNDQGITNKCKMNLQDNNGNDIGFI
sp Q45894 BXA2_CLOBO	GVEKILSALEIPDVGNLSQVVMKSKDDQGIRNKCKMNLQDNNGNDIGFI
tr Q58GH1 Q58GH1_CLOBO	GVEKILSALEIPDVGNLSQVVMKSKDDQGIRNKCKMNLQDNNGNDIGFI *****:*****
sp P10845 BXA1_CLOBO	GFHQFNNAKLVASNWNRYRQIERSSRTLGCSEFIPVDDGWGERPL
tr Q7B8V4 Q7B8V4_CLOBO	GFHQFNNAKLVASNWNRYRQIERSSRTLGCSEFIPVDDGWGERPL
sp Q45894 BXA2_CLOBO	GFHLYDNIKLVASNWNRYRQVGKASRTFGCSEFIPVDDGWGESL
tr Q58GH1 Q58GH1_CLOBO	GFHLYDNIKLVASNWNRYRQVGKASRTFGCSEFIPVDDGWGESL *** :*****:***:***** *

FileUp

MSF: 1296 Type: P Check: 8703 ..

Name: sp|P10845|BXA1_CLOBO oo Len: 1296 Check: 7638 Weight: 0.100
 Name: tr|Q7B8V4|Q7B8V4_CLOBO oo Len: 1296 Check: 7102 Weight: 0.100
 Name: sp|Q45894|BXA2_CLOBO oo Len: 1296 Check: 1966 Weight: 0.100
 Name: tr|Q58GH1|Q58GH1_CLOBO oo Len: 1296 Check: 1997 Weight: 0.100

//

sp P10845 BXA1_CLOBO	.PFVNKQFNY	KDPVNGVDIA	YIKIPNVGQM	QPVKAFKIHN	KIWWIPERDT
tr Q7B8V4 Q7B8V4_CLOBO	MPFVNKQFNY	KDPVNGVDIA	YIKIPNAGQM	QPVKAFKIHN	KIWWIPERDT
sp Q45894 BXA2_CLOBO	.PFVNKQFNY	KDPVNGVDIA	YIKIPNAGQM	QPVKAFKIHN	KIWWIPERDT
tr Q58GH1 Q58GH1_CLOBO	MPFVNKQFNY	KDPVNGVDIA	YIKIPNAGQM	QPVKAFKIHN	KIWWIPERDT

sp P10845 BXA1_CLOBO	FTNPEEGDLN	PPPEAKQVPV	SYYDSTYLST	DNEKDNYLKG	VTKLFERIYS
tr Q7B8V4 Q7B8V4_CLOBO	FTNPEEGDLN	PPPEAKQVPV	SYYDSTYLST	DNEKDNYLKG	VTKLFERIYS
sp Q45894 BXA2_CLOBO	FTNPEEGDLN	PPPEAKQVPV	SYYDSTYLST	DNEKDNYLKG	VTKLFERIYS
tr Q58GH1 Q58GH1_CLOBO	FTNPEEGDLN	PPPEAKQVPV	SYYDSTYLST	DNEKDNYLKG	VTKLFERIYS

sp P10845 BXA1_CLOBO	TDLGRMLLTS	IVRGIPFWGG	STIDTELKVI	DTNCINVIQP	DGSYRSEELN
tr Q7B8V4 Q7B8V4_CLOBO	TDLGRMLLTS	IVRGIPFWGG	STIDTELKVI	DTNCINVIQP	DGSYRSEELN
sp Q45894 BXA2_CLOBO	TDLGRMLLTS	IVRGIPFWGG	STIDTELKVI	DTNCINVIQP	DGSYRSEELN
tr Q58GH1 Q58GH1_CLOBO	TDLGRMLLTS	IVRGIPFWGG	STIDTELKVI	DTNCINVIQP	DGSYRSEELN

sp P10845 BXA1_CLOBO	LVIIGPSADI	IQFECKSFGE	EVLNLTRNGY	GSTQYIRFSP	DFTFGFEESL
tr Q7B8V4 Q7B8V4_CLOBO	LVIIGPSADI	IQFECKSFGE	EVLNLTRNGY	GSTQYIRFSP	DFTFGFEESL
sp Q45894 BXA2_CLOBO	LVIIGPSADI	IQFECKSFGE	DVLNLTRNGY	GSTQYIRFSP	DFTFGFEESL
tr Q58GH1 Q58GH1_CLOBO	LVIIGPSADI	IQFECKSFGE	DVLNLTRNGY	GSTQYIRFSP	DFTFGFEESL

sp P10845 BXA1_CLOBO	EVDTNPLLGA	GKFATDPAVT	LAHELIHAGH	RLYGIAINPN	RVFKVNTNAY
tr Q7B8V4 Q7B8V4_CLOBO	EVDTNPLLGA	GKFATDPAVT	LAHELIHAGH	RLYGIAINPN	RVFKVNTNAY
sp Q45894 BXA2_CLOBO	EVDTNPLLGA	GKFATDPAVT	LAHELIHAEH	RLYGIAINPN	RVFKVNTNAY
tr Q58GH1 Q58GH1_CLOBO	EVDTNPLLGA	GKFATDPAVT	LAHELIHAEH	RLYGIAINPN	RVFKVNTNAY

sp P10845 BXA1_CLOBO	YEMSGLEVSF	EELRTFGGHD	AKFIDSLQEN	EFRLYYYNKF	KDIASTLNKA
tr Q7B8V4 Q7B8V4_CLOBO	YEMSGLEVSF	EELRTFGGHD	AKFIDSLQEN	EFRLYYYNKF	KDIASTLNKA
sp Q45894 BXA2_CLOBO	YEMSGLEVSF	EELRTFGGHD	AKFIDSLQEN	EFRLYYYNKF	KDVASTLNKA
tr Q58GH1 Q58GH1_CLOBO	YEMSGLEVSF	EELRTFGGHD	AKFIDSLQEN	EFRLYYYNKF	KDVASTLNKA

sp P10845 BXA1_CLOBO	KSIVGTTASL	QYMKNVFKEK	YLLSEDTSKG	FSVDKLKFDK	LYKMLTEIYT
tr Q7B8V4 Q7B8V4_CLOBO	KSIVGTTASL	QYMKNVFKEK	YLLSEDTSKG	FSVDKLKFDK	LYKMLTEIYT
sp Q45894 BXA2_CLOBO	KSIIGTTASL	QYMKNVFKEK	YLLSEDTSKG	FSVDKLKFDK	LYKMLTEIYT
tr Q58GH1 Q58GH1_CLOBO	KSIIGTTASL	QYMKNVFKEK	YLLSEDTSKG	FSVDKLKFDK	LYKMLTEIYT

sp P10845 BXA1_CLOBO	EDNFVKFFKV	LNRKTYLNFD	KAVFKINIVP	KVNYTIYDGF	NLRNTNLAAN
tr Q7B8V4 Q7B8V4_CLOBO	EDNFVKFFKV	LNRKTYLNFD	KAVFKINIVP	KVNYTIYDGF	NLRNTNLAAN
sp Q45894 BXA2_CLOBO	EDNFVNFFKV	INRKTYLNFD	KAVFRINIVP	DENYTIKDG	NLKGANLSTN

tr Q58GH1 Q58GH1_CLOBO	EDNFVNFFKV INRKTYLNFD KAVFRINIVP DENYTIKDGf NLKGANLSTN
sp P10845 BXA1_CLOBO	FNGQNTTEINN MNFTKLKNFT GLFEFYKLLC VRGIITSKTK SLDKGYNKAL
tr Q7B8V4 Q7B8V4_CLOBO	FNGQNTTEINN MNFTKLKNFT GLFEFYKLLC VRGIITSKTK SLDKGYNKAL
sp Q45894 BXA2_CLOBO	FNGQNTTEINS RNFTRLKNFT GLFEFYKLLC VRGIIPFKTK SLDEGYNKAL
tr Q58GH1 Q58GH1_CLOBO	FNGQNTTEINS RNFTRLKNFT GLFEFYKLLC VRGIIPFKTK SLDEGYNKAL
sp P10845 BXA1_CLOBO	NDLCIKVNNW DLFFSPSEDN FTNDLNKGEE ITSdTNIeAA EENISLDLIQ
tr Q7B8V4 Q7B8V4_CLOBO	NDLCIKVNNW DLFFSPSEDN FTNDLNKGEE ITSdTNIeAA EENISLDLIQ
sp Q45894 BXA2_CLOBO	NDLCIKVNNW DLFFSPSEDN FTNDLDKVEE ITADTNIEAA EENISLDLIQ
tr Q58GH1 Q58GH1_CLOBO	NDLCIKVNNW DLFFSPSEDN FTNDLDKVEE ITADTNIEAA EENISLDLIQ
sp P10845 BXA1_CLOBO	QYYLTFNFDN EPENISIEENL SSDIIGQLEL MPNIERFPNG KKYELDKYTM
tr Q7B8V4 Q7B8V4_CLOBO	QYYLTFNFDN EPENISIEENL SSDIIGQLEL MPNIERFPNG KKYELDKYTM
sp Q45894 BXA2_CLOBO	QYYLTFDFDN EPENISIEENL SSDIIGQLEP MPNIERFPNG KKYELDKYTM
tr Q58GH1 Q58GH1_CLOBO	QYYLTFDFDN EPENISIEENL SSDIIGQLEP MPNIERFPNG KKYELDKYTM
sp P10845 BXA1_CLOBO	FHYLRAQEFf HGKSRIALTn SVNEALLNPS RVYTFfSSDY VKKVNKATEA
tr Q7B8V4 Q7B8V4_CLOBO	FHYLRAQEFf HGKSRIALTn SVNEALLNPS RVYTFfSSDY VKKVNKATEA
sp Q45894 BXA2_CLOBO	FHYLRAQEFf HGDSRIILTn SAEeALLKPN VAYTFfSSKY VKKINKAVEA
tr Q58GH1 Q58GH1_CLOBO	FHYLRAQEFf HGDSRIILTn SAEeALLKPN VAYTFfSSKY VKKINKAVEA
sp P10845 BXA1_CLOBO	AMFLGWVEQL VYDfTDEtSE VSTTDKIADI TIIPYIGPA LNIGNMLYKD
tr Q7B8V4 Q7B8V4_CLOBO	AMFLGWVEQL VYDfTDEtSE VSTTDKIADI TIIPYIGPA LNIGNMLYKD
sp Q45894 BXA2_CLOBO	FMFLNWAEEL VYDfTDEtNE VTTMDKIADI TIIVPYIGPA LNIGNMLSKG
tr Q58GH1 Q58GH1_CLOBO	FMFLNWAEEL VYDfTDEtNE VTTMDKIADI TIIVPYIGPA LNIGNMLSKG
sp P10845 BXA1_CLOBO	DFVGALIFSG AVILLEFIPE IAIPVLGTfA LVSYIANKVL TVQTIDNALS
tr Q7B8V4 Q7B8V4_CLOBO	DFVGALIFSG AVILLEFIPE IAIPVLGTfA LVSYIANKVL TVQTIDNALS
sp Q45894 BXA2_CLOBO	EFVEAIIFTG VVAMLEFIPE YALPVFGTfA IVSYIANKVL TVQTINNALS
tr Q58GH1 Q58GH1_CLOBO	EFVEAIIFTG VVAMLEFIPE YALPVFGTfA IVSYIANKVL TVQTINNALS
sp P10845 BXA1_CLOBO	KRNEKWDEVY KYIVTNWLAK VNTQIDLIRK KMKEALENQA EATKAiINYQ
tr Q7B8V4 Q7B8V4_CLOBO	KRNEKWDEVY KYIVTNWLAK VNTQIDLIRK KMKEALENQA EATKAiINYQ
sp Q45894 BXA2_CLOBO	KRNEKWDEVY KYTVTNWLAK VNTQIDLIRE KMKKALENQA EATKAiINYQ
tr Q58GH1 Q58GH1_CLOBO	KRNEKWDEVY KYTVTNWLAK VNTQIDLIRE KMKKALENQA EATKAiINYQ
sp P10845 BXA1_CLOBO	YNQYTEEEKN NINFNIDDLs SKLNESINKA MININKFLNq CSVSYLMNSM
tr Q7B8V4 Q7B8V4_CLOBO	YNQYTEEEKN NINFNIDDLs SKLNESINKA MININKFLNq CSVSYLMNSM
sp Q45894 BXA2_CLOBO	YNQYTEEEKN NINFNIDDLs SKLNESINSA MININKFLDQ CSVSYLMNSM
tr Q58GH1 Q58GH1_CLOBO	YNQYTEEEKN NINFNIDDLs SKLNESINSA MININKFLDQ CSVSYLMNSM
sp P10845 BXA1_CLOBO	IPYGVKRLed FDASLKDALL KYIYDNRGTL IGQVDRlKDK VNNTLSTDiP
tr Q7B8V4 Q7B8V4_CLOBO	IPYGVKRLed FDASLKDALL KYIYDNRGTL IGQVDRlKDK VNNTLSTDiP
sp Q45894 BXA2_CLOBO	IPYAVKRLKd FDASVRDVLl KYIYDNRGTL VLQVDRlKDE VNNTLSADiP
tr Q58GH1 Q58GH1_CLOBO	IPYAVKRLKd FDASVRDVLl KYIYDNRGTL VLQVDRlKDE VNNTLSADiP
sp P10845 BXA1_CLOBO	FQLSKYVDNq RLLSTfTEYI KNIINTSiLlN LRYESNHLID LSRYASKiNi
tr Q7B8V4 Q7B8V4_CLOBO	FQLSKYVDNq RLLSTfTEYI KNIINTSiLlN LRYESNHLID LSRYASKiNi
sp Q45894 BXA2_CLOBO	FQLSKYVDNK KLLSTfTEYI KNiVNTSiLS iVYKKDDLiD LSRYGAKiNi

tr	Q58GH1	Q58GH1_CLOBO	FQLSKYVDNK	KLLSTFTEYI	KNIVNTSILS	IVYKKDDLID	LSRYGAKINI
sp	P10845	BXA1_CLOBO	GSKVNFDPID	KNQIQLFNLE	SSKIEVILKN	AIVYNSMYEN	FSTSFWIRIP
tr	Q7B8V4	Q7B8V4_CLOBO	GSKVNFDPID	KNQIQLFNLE	SSKIEVILKN	AIVYNSMYEN	FSTSFWIRIP
sp	Q45894	BXA2_CLOBO	GDRVYYSID	KNQIKLINLE	SSTIEVILKN	AIVYNSMYEN	FSTSFWIKIP
tr	Q58GH1	Q58GH1_CLOBO	GDRVYYSID	KNQIKLINLE	SSTIEVILKN	AIVYNSMYEN	FSTSFWIKIP
sp	P10845	BXA1_CLOBO	KYFNSISLNN	EYTIINCMEN	NSGWKVSILNY	GEIIWTLQDT	QEIQRVVFKE
tr	Q7B8V4	Q7B8V4_CLOBO	KYFNSISLNN	EYTIINCMEN	NSGWKVSILNY	GEIIWTLQDT	QEIQRVVFKE
sp	Q45894	BXA2_CLOBO	KYFSKINLNN	EYTIINCIEN	NSGWKVSILNY	GEIIWTLQDN	KQNIQRVVFKE
tr	Q58GH1	Q58GH1_CLOBO	KYFSKINLNN	EYTIINCIEN	NSGWKVSILNY	GEIIWTLQDN	KQNIQRVVFKE
sp	P10845	BXA1_CLOBO	YSQMINISDY	INRWIFVTIT	NNRLNNSKIY	INGRLIDQKP	ISNLGNIHAS
tr	Q7B8V4	Q7B8V4_CLOBO	YSQMINISDY	INRWIFVTIT	NNRLNNSKIY	INGRLIDQKP	ISNLGNIHAS
sp	Q45894	BXA2_CLOBO	YSQMVNISDY	INRWIFVTIT	NNRLTKSKIY	INGRLIDQKP	ISNLGNIHAS
tr	Q58GH1	Q58GH1_CLOBO	YSQMVNISDY	INRWIFVTIT	NNRLTKSKIY	INGRLIDQKP	ISNLGNIHAS
sp	P10845	BXA1_CLOBO	NNIMFKLDGC	RDTHRYIWIK	YFNLFDEKELN	EKEIKDLYDN	QNSNGILKDF
tr	Q7B8V4	Q7B8V4_CLOBO	NNIMFKLDGC	RDTHRYIWIK	YFNLFDEKELN	EKEIKDLYDN	QNSNGILKDF
sp	Q45894	BXA2_CLOBO	NKIMFKLDGC	RDPRRYIMIK	YFNLFDEKELN	EKEIKDLYDS	QNSNGILKDF
tr	Q58GH1	Q58GH1_CLOBO	NKIMFKLDGC	RDPRRYIMIK	YFNLFDEKELN	EKEIKDLYDS	QNSNGILKDF
sp	P10845	BXA1_CLOBO	WGDYLYQYDKP	YYMLNLDPN	KYVDVNNVGI	RGYMYLKGPR	GSVMTTNIYL
tr	Q7B8V4	Q7B8V4_CLOBO	WGDYLYQYDKP	YYMLNLDPN	KYVDVNNVGI	RGYMYLKGPR	GSVMTTNIYL
sp	Q45894	BXA2_CLOBO	WGNLYQYDKP	YYMLNLDPN	KYVDVNNIGI	RGYMYLKGPR	GSVVTTNIYL
tr	Q58GH1	Q58GH1_CLOBO	WGNLYQYDKP	YYMLNLDPN	KYVDVNNIGI	RGYMYLKGPR	GSVVTTNIYL
sp	P10845	BXA1_CLOBO	NSSLYRGTKF	IIKKYASGNK	DNIVRNNDRV	YINVVVKNE	YRLATNASQA
tr	Q7B8V4	Q7B8V4_CLOBO	NSSLYRGTKF	IIKKYASGNK	DNIVRNNDRV	YINVVVKNE	YRLATNASQA
sp	Q45894	BXA2_CLOBO	NSTLYEGTKF	IIKKYASGNE	DNIVRNNDRV	YINVVVKNE	YRLATNASQA
tr	Q58GH1	Q58GH1_CLOBO	NSTLYEGTKF	IIKKYASGNE	DNIVRNNDRV	YINVVVKNE	YRLATNASQA
sp	P10845	BXA1_CLOBO	GVEKILSALE	IPDVGNLSQV	VVMKSKNDQG	ITNKCKMNLQ	DNNGNDIGFI
tr	Q7B8V4	Q7B8V4_CLOBO	GVEKILSALE	IPDVGNLSQV	VVMKSKNDQG	ITNKCKMNLQ	DNNGNDIGFI
sp	Q45894	BXA2_CLOBO	GVEKILSALE	IPDVGNLSQV	VVMKSKDDQG	IRNKCKMNLQ	DNNGNDIGFI
tr	Q58GH1	Q58GH1_CLOBO	GVEKILSALE	IPDVGNLSQV	VVMKSKDDQG	IRNKCKMNLQ	DNNGNDIGFI
sp	P10845	BXA1_CLOBO	GFHQFNNAK	LVASNWNQ	IERSSRTLGC	SWEFIPVDDG	WGERPL
tr	Q7B8V4	Q7B8V4_CLOBO	GFHQFNNAK	LVASNWNQ	IERSSRTLGC	SWEFIPVDDG	WGERPL
sp	Q45894	BXA2_CLOBO	GFHLYDNIAK	LVASNWNQ	VGKASRTFGC	SWEFIPVDDG	WGESL
tr	Q58GH1	Q58GH1_CLOBO	GFHLYDNIAK	LVASNWNQ	VGKASRTFGC	SWEFIPVDDG	WGESL

sp P10845 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA1_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 868 bits (2243), Expect = 0.0
 Identities = 423/423 (100%), Positives = 423/423 (100%)

Query: 1 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
 Sbjct: 873 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 932

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI
 Sbjct: 933 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 992

Query: 121 KQRVVFKEYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 KQRVVFKEYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
 Sbjct: 993 KQRVVFKEYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 1052

Query: 181 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM 240
 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM
 Sbjct: 1053 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM 1112

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI
 Sbjct: 1113 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 1172

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITN 360
 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITN
 Sbjct: 1173 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITN 1232

Query: 361 KCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGC SWEFIPVDDGWGE 420
 KCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGC SWEFIPVDDGWGE
 Sbjct: 1233 KCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGC SWEFIPVDDGWGE 1292

Query: 421 RPL 423
 RPL
 Sbjct: 1293 RPL 1295

tr Q7B8V4 BoNT/A (Neurotoxin BoNT) [bont/a] [Clostridium 1296
 Q7B8V4_CLOBO botulinum] AA
 align

Score = 868 bits (2243), Expect = 0.0
 Identities = 423/423 (100%), Positives = 423/423 (100%)

Query: 1 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
 Sbjct: 874 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 933

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI
 Sbjct: 934 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 993

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
 Sbjct: 994 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 1053

Query: 181 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM 240
 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM
 Sbjct: 1054 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM 1113

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI
 Sbjct: 1114 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 1173

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 360
 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN
 Sbjct: 1174 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 1233

Query: 361 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCSEWEIFVDDGWGE 420
 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCSEWEIFVDDGWGE
 Sbjct: 1234 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCSEWEIFVDDGWGE 1293

Query: 421 RPL 423
 RPL
 Sbjct: 1294 RPL 1296

sp Q45894 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA2_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 765 bits (1976), Expect = 0.0
 Identities = 368/423 (86%), Positives = 397/423 (92%)

Query: 1 INTSILNLRYESNHLIDL SRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 +NTSIL++ Y+ + LIDLSRY +KINIG +V +D IDKNQI+L NLESS IEVILKNAIV
 Sbjct: 873 VNTSILSIVYKKDDLIDL SRYGAKINIGDRVYYSIDKNQIKLINLESSTIEVILKNAIV 932

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINC MENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWI+IPKYF+ I+LNNEYTIINC+ENNSGWKVS LNYGEIIWTLQD ++
 Sbjct: 933 YNSMYENFSTSFWIKIPKYFSKINLNNEYTIINCIENNSGWKVS LNYGEIIWTLQDNKQN 992

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 QRVVVFYKYSQMNISDYINRWIFVTITNNRL SKIYINGRLIDQKPISNLGNIHASN I
 Sbjct: 993 IQRVVFYKYSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKI 1052

Query: 181 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM 240
 MFKLDGCRD RYI IKYFNLFDKELNEKEIKDLYD+QSN SGILKDFWG+YLQYDKPYM
 Sbjct: 1053 MFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSN SGILKDFWGNLYLQYDKPYM 1112

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
 LNL+DPNKYVDVNN+GIRGYMYLKGPRGSV+TTNIYLN S+LY GTKFIIKKYASGN+DNI
 Sbjct: 1113 LNLDPNKYVDVNNIGIRGYMYLKGPRGSVTTNIYLNSTLYEGTKFIIKKYASGNEDNI 1172

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 360
 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSK+DQGI N

Sbjct: 1173 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRN 1232

Query: 361 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEFIPVDDGWGE 420
KCKMNLQDNNNGNDIGFIGFH ++NIAKLVASNWNRYRQ+ ++SRT GCSWEFIPVDDGWGE

Sbjct: 1233 KCKMNLQDNNNGNDIGFIGFHLVDNIAKLVASNWNRYRQVGKASRTFGCSWEFIPVDDGWGE 1292

Query: 421 RPL 423
L

Sbjct: 1293 SSL 1295

tr Q58GH1 Type A2 botulinum neurotoxin [Clostridium botulinum] 1296 AA
Q58GH1_CLOBO

align

Score = 765 bits (1976), Expect = 0.0
Identities = 368/423 (86%), Positives = 397/423 (92%)

Query: 1 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
+NTSIL++ Y+ + LIDLRLRY +KINIG +V +D IDKNQI+L NLESS IEVILKNAIV

Sbjct: 874 VNTSILSIVYKDDIDLRLRYGAKINIGDRVYDSIDKNQIKLINLESSTIEVILKNAIV 933

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINC MENNSGWKVS LN YGEIIWTLQDTQEI 120
YNSMYENFSTSFWRIPKYF+ I+LNNEYTIINC+ENNSGWKVS LN YGEIIWTLQD ++

Sbjct: 934 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINC IENNSGWKVS LN YGEIIWTLQDNKQN 993

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
QRVVFYKYSQMINISDYINRWIFVTITNNRL SKIYINGRLIDQKPISNLGNIHASN I

Sbjct: 994 IQRVVFYKYSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKI 1053

Query: 181 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM 240
MFKLDGCRD RYI IKYFNLFDKELNEKEIKDLYD+QSN SGILKDFWG+YLYQDKPYM

Sbjct: 1054 MFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSN SGILKDFWGNLYQDKPYM 1113

Query: 241 LNLDPN KYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
LNL+DPN KYVDVNN+GIRGYMYLKGPRGSV+TTNIYLN S+LY GTKFIIKKYASGN+DNI

Sbjct: 1114 LNLDPN KYVDVNNIGIRGYMYLKGPRGSVMTTNIYLNSTLYEGTKFIIKKYASGNEDNI 1173

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITN 360
VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSK+DQGI N

Sbjct: 1174 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRN 1233

Query: 361 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEFIPVDDGWGE 420
KCKMNLQDNNNGNDIGFIGFH ++NIAKLVASNWNRYRQ+ ++SRT GCSWEFIPVDDGWGE

Sbjct: 1234 KCKMNLQDNNNGNDIGFIGFHLVDNIAKLVASNWNRYRQVGKASRTFGCSWEFIPVDDGWGE 1293

Query: 421 RPL 423
L

Sbjct: 1294 SSL 1296